

User Manual for NetworkDistances 1.0: Calculating Network-wise Distances Between Habitat Patches for Spatially Restricted Species

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SPECIES

by

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ABSTRACT

Grinnell, M.H. and Curtis, J.M.R. 2011. User manual for NetworkDistances 1.0: Calculating network-wise distances between habitat patches for spatially restricted species. Can. Tech. Rep. Fish. Aquat. Sci. 2960: iv + 29 p.

We develop an approach to calculate distances along network lines between habitat patches using **NetworkDistances** version 1.0. The **NetworkDistances** code is an optional extension to the **GRIP2** script for species that are restricted to moving along defined networks (e.g., rivers). For these species, the Euclidean distance may underestimate the actual distance between patches, which may influence patch dynamics. To more accurately reflect reality, we calculate the shortest 'along the network' distance between connected patches using **NetworkDistances**, and apply our analysis to a stream-dwelling minnow, the redside dace (*Clinostomus elongatus*).

RÉSUMÉ

Grinnell, M.H. and Curtis, J.M.R. 2011. User manual for NetworkDistances 1.0: Calculating network-wise distances between habitat patches for spatially restricted species. Can. Tech. Rep. Fish. Aquat. Sci. 2960: iv + 29 p.

Nous avons élaboré une méthode de calcul des distances le long des lignes de réseaux entre les parcelles d'habitat au moyen de la version 1.0 de **NetworkDistances**. Le code de **NetworkDistances** est une extension optionnelle du script **GRIP2**, utilisé pour les espèces dont les déplacements sont limités le long de réseaux définis (p. ex. des rivières). Pour ces espèces, la distance euclidienne peut sous-estimer la distance réelle entre les parcelles, ce qui peut influer sur la dynamique des parcelles. Pour refléter la réalité avec plus de justesse, nous calculons la distance la plus courte « le long du réseau » entre les parcelles reliées au moyen de **NetworkDistances**, puis nous appliquons notre analyse à un méné fréquentant les cours d'eau du réseau, soit le méné long (*Clinostomus elongatus*).

1 MOTIVATION

A *metapopulation* consists of multiple spatially discrete populations that occasionally exchange organisms, even though each population is in a discrete habitat patch. Organisms may move between patches when distances are less than the maximum dispersal distance, and dispersal success is typically inversely related to dispersal distance (Wolfenbarger 1946; Kitching 1971). The exchange of organisms between patches can affect patch dynamics and metapopulation persistence via patch recolonization and extinction rates (Johst et al. 2002). Dispersal rates among patches are typically modeled as a function of distance and cost(s) associated with moving through suboptimal habitat within a landscape or seascape. For some species, the Euclidean (i.e., straight line) distance may be appropriate for modeling the migration distance between patches. However, landscape features may prevent other species from moving in a straight line between patches (Figure 1). For these spatially restricted species, the Euclidean distance may under-estimate the effective distance between patches, as well as over-estimate migration rates and dispersal success, leading to biases in predicted patch extinction and recolonization rates.

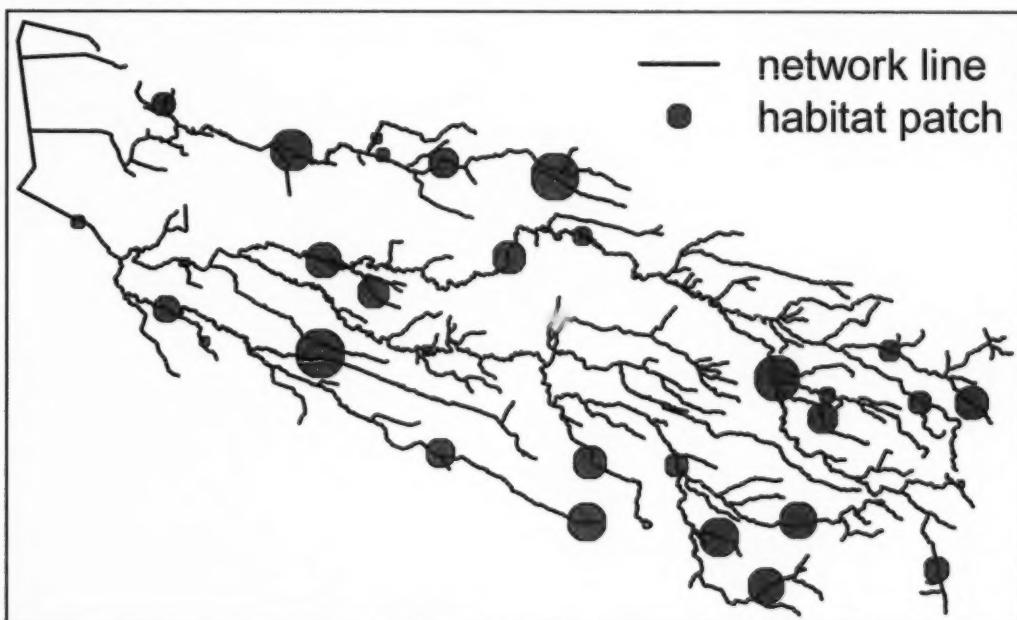


Figure 1. Hypothetical landscape for a lotic species that is restricted to moving along network lines (e.g., rivers) that connect patches of suitable habitat (e.g., riffles). Note that patch size is proportional to circle size.

2 BACKGROUND

We assume that readers contemplating use of the **NetworkDistances** code are familiar with the suite of **RAMAS** software, specifically **RAMAS GIS** and **Metapop** (Akçakaya 2005) as well as **GRIP** (Curtis and Naujokaitis-Lewis 2008a,b). Briefly, the **GRIP2** script, written in the programming language **R** (RDCT 2011), is designed for use with **RAMAS GIS 5.0** software to perform systematic global sensitivity analysis of habitat and population parameters for spatially explicit population viability analyses. The **RAMAS GIS** programme links spatial data (e.g., habitat suitability maps) to stochastic metapopulation models, and allows users to evaluate the influence of landscape structure on metapopulation dynamics by manually varying habitat parameters. The **GRIP2** script automates this time-consuming process by generating a specified number of random sets of spatial and non-spatial parameters, and running these iterations by submitting batch files to **RAMAS**. By default, **GRIP2** and **RAMAS** software calculate the Euclidean distance between patches.

We developed **NetworkDistances** version 1.0, an optional **GRIP2** extension, to be used when organism movement and dispersal is restricted to defined spatial networks (Figure 2). For example, the movement of lotic fish is restricted to river networks, while other species may be restricted to moving along hedgerows, coastlines, trails, or corridors. Specifically, we developed **NetworkDistances** to automate the calculation of distances between pairs of patches for redside dace (RSD; *Clinostomus elongatus*), an Endangered stream-dwelling minnow found *inter alia* in four watersheds in the Greater Toronto Area that discharge into Lake Ontario, Canada (COSEWIC 2007). We provide some background information on RSD and refer to features of our RSD model in this manual to illustrate concepts, limitations, and opportunities where appropriate. Most code within **NetworkDistances** is generic and could be applied to any spatially-constrained species to calculate pairwise distances. We attempt to highlight sections of code that may require some customization for application with other species.

The **NetworkDistances** code (**NetworkDistances.R**) has extensive comments and should be referenced when reading this document. Please contact the authors if you have questions, comments, suggestions or concerns regarding the manual, or the code. We are attempting to keep track of this code's use; please cite this manual and contact the authors if you use **NetworkDistances**. Note that **NetworkDistances** comes with absolutely no warranty.

3 RSD HABITAT AND NETWORK DATA

River data were acquired from Natural Resources Canada as a vector line shapefile (scale = 1: 50 000; NRC 2011). Georeferenced shapefiles for RSD habitat patches and rivers were projected in Universal Transverse Mercator (UTM, zone 17), in metres (m) using the North American 1983 datum. Data preparation for **RAMAS** input files (e.g., habitat mask, habitat suitability grid) was done using the geographic information system programme **ArcMap 9.2** (ESRI 2006). Although spatial files for **RAMAS** input

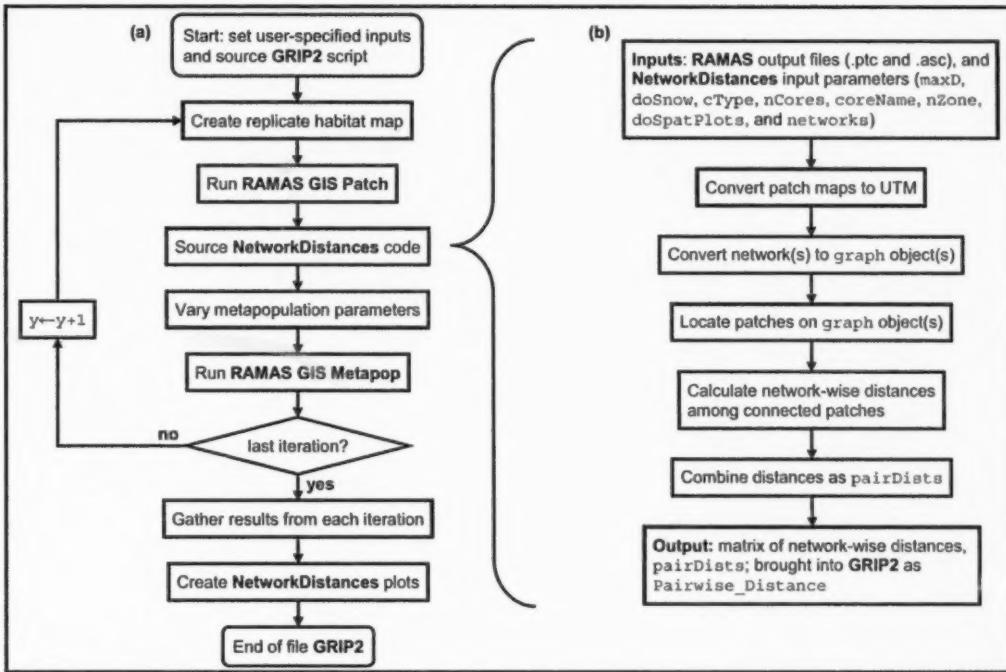


Figure 2. Simplified flow diagram of the **GRIP2** script (a), and the optional **NetworkDistances** code (b). The **NetworkDistances** algorithm is expanded in Subsection 4.2, and inputs are described in Section 5.

(e.g., ***.asc**) must have, *inter alia*, consistent precision and spatial extent (Akçakaya 2005), networks may extend beyond the grid's perimeter. However, larger networks may increase memory and processing time, as discussed in Subsection 4.1.

In our case study, we modeled the metapopulation dynamics of RSD within a small study area, which contains two watersheds (Figure 3). Two RSD characteristics enabled us to simplify our analysis, and thus our code. First, genetic analyses indicate that RSD do not move between watersheds (M. Poos, unpublished data), which allowed us to divide the study area into two independent watersheds, which we refer to as *networks*. We defined individual networks by their Strahler stream order number, a measure of branching complexity (Strahler 1957). Second, mark-recapture studies indicate that RSD dispersal is independent of stream direction (Poos and Jackson, *in press*), which allowed us to create undirected **graph** objects. The benefits of these two simplifications are explained in later sections.

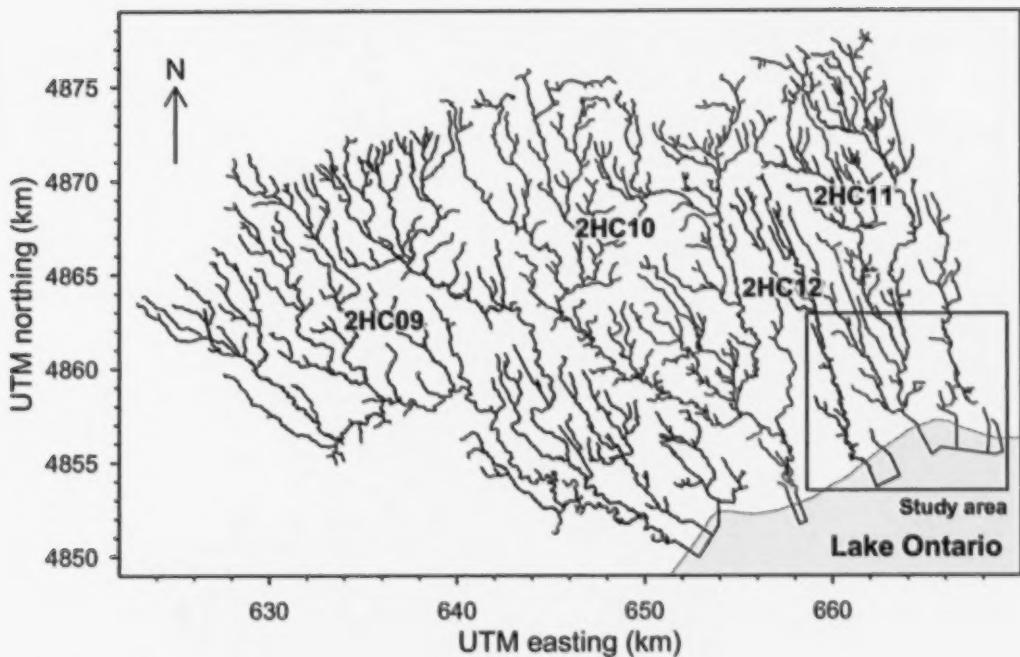


Figure 3. Two of the four watersheds (e.g., 2HC11) run through the redeye dace study area, and discharge into Lake Ontario (NRC 2011). Geographic coordinates are projected in Universal Transverse Mercator (UTM, zone 17), in kilometres (km). Note that networks are different colours to aid with differentiation.

4 METHODOLOGY USING R

We assume the user has at least a working ability with the **R** statistical and graphing programme (RDCT 2011), and is familiar with spatial data. In addition to the **R** packages required for **GRIP2** [sp (Pebesma and Bivand 2005; Bivand et al. 2008), rgdal (Keitt et al. 2010), spatial (Venables and Ripley 2002), spatstat (Baddeley and Turner 2005), adehabitat (Calenge 2006), maptools (Lewin-Koh and Bivand 2011), ade4 (Dray and Dufour 2007), and gplib (Peng 2010)], **NetworkDistances** requires at least five additional packages: PBSmapping (Schnute et al. 2010) to handle georeferenced data; graph (Gentleman et al. 2010), RBGL (Carey et al. 2010), and igraph (Csárdi and Nepusz 2006) to handle graph objects; as well as gtools (Warnes 2010) to sort strings with embedded numbers. One or two other packages are optional: snow (Tierney et al. 2008) to use multiple processors; and (also optionally) Rmpi (Yu 2010) to use “MPI” type clusters on non-Windows machines. Non-Windows machines require additional code to ensure that files are compatible with both dos and unix, as well as the **WineHQ** programme (WPD 2010) to run **RAMAS** if **NetworkDistances** is used along with **GRIP2**.

4.1 CHALLENGES AND SOLUTIONS TO MEMORY AND TIME REQUIREMENTS

The main challenge to **NetworkDistances** is that large, complex networks with many patches and high resolution maps may be costly in terms of required memory and processing time. However, memory and time requirements can be reduced significantly using four strategies: (1) splitting large networks into independent sub-networks; (2) loading saved RData objects from the first iteration; (3) parallel processing; and (4) reducing map resolution.

First, large networks will require less memory and processing time if they can be split into independent sub-networks in a biologically meaningful way. Splitting a large network (within which some patches are not connected) into multiple sub-networks (within which all patches are connected) reduces the number of pairwise distance calculations. For example, because RSD do not migrate between watersheds, we split the large river network in our study area into two small independent networks by watershed boundaries (Figure 3). More generally, consider a hypothetical scenario with three patches on one network (e.g., patches *a*, *b*, *c*), and three patches on a second, independent network (e.g., *d*, *e*, *f*). Treated as one large network, there are 15 pairwise distances to calculate for the upper triangle of the required 6×6 matrix:

	<i>a</i>	<i>b</i>	<i>c</i>	<i>d</i>	<i>e</i>	<i>f</i>	
<i>a</i>	0	1	2	NA	NA	NA	
<i>b</i>	1	0	3	NA	NA	NA	
<i>c</i>	2	3	0	NA	NA	NA	
<i>d</i>	NA	NA	NA	0	4	5	
<i>e</i>	NA	NA	NA	4	0	6	
<i>f</i>	NA	NA	NA	5	6	0	

(1)

where “NA” indicates that the distance cannot be calculated because the two patches are unconnected (i.e., due to migration barriers between patches).³ Note that the lower triangle is the transpose of the upper triangle because dispersal is assumed to be independent of direction. Alternately, treating the two sub-networks independently reduces the number of pairwise distance calculations from 15 to 6, all of which can be calculated:

<i>a</i>	<i>b</i>	<i>c</i>		<i>d</i>	<i>e</i>	<i>f</i>		
<i>a</i>	0	1	2		<i>d</i>	0	4	5
<i>b</i>	1	0	3	and	<i>e</i>	4	0	6
<i>c</i>	2	3	0		<i>f</i>	5	6	0

(2)

To further reduce network sizes, we then removed sections outside the study area boundary.

³The algorithm requires more time and memory to attempt to calculate distances between unconnected patches than connected patches, and eventually sets these distances to NA.

Second, as a sensitivity analysis programme, **GRIP2** typically runs multiple iterations, and network lines remain constant from one iteration to another. Thus, networks can be saved to disk as **RData** objects on the first iteration, and loaded from disk on subsequent iterations. This strategy reduces processing time considerably for large networks. However, due to changing patch locations associated with random changes in landscape structure each iteration, pairwise distances must be calculated iteratively.

Third, calculating pairwise distances can be computationally demanding, and takes considerable time when networks are large, or when there are many patches. In these cases, calculating pairwise distances requires more processing time than creating networks, and multiple processors can be used to reduce processing time. In this case, the **NetworkDistances** code starts multiple instances of **R**, and divides pairwise distance calculations among processors on the cluster. With sufficient memory, parallel processing may even reduce processing time on computers with only one processor.

Finally, time and memory requirements increase in proportion to increasing network size, branching complexity, number of pairwise distance calculations, and size of input maps. Processing time and memory requirements were considerable because the RSD study area was modeled at a fine spatial resolution: our input maps have approximately 443 000 15 m × 15 m grid cells. For example, between 1.0 and 1.5 hours were required to run 50 **GRIP2** iterations of the RSD study area on two different machines. Of the total required time, between 2.8 and 5.2% was used to run the **NetworkDistances** code. Our analysis required fine spatial resolution because RSD are typically distributed in headwater streams that are closely spaced, but networks for other species may not require such fine spatial resolution.

4.2 OUTLINE OF THE **NetworkDistances** CODE

Our analysis relies on well-developed methods from graph theory to measure distances between patches along networks. Although graph theory has been around for many years, using graphs to model node (e.g., patch) connectivity is relatively new to the field of conservation biology (Urban et al. 2009). We developed the **NetworkDistances** code in the programming language **R** to facilitate implementation with **GRIP2**, and to cope with changing patch locations each iteration.

The **NetworkDistances** code is typically sourced via the **GRIP2** script for spatially restricted species, and we assume that the user is familiar with **GRIP2**. Alternately, **NetworkDistances** can be run independently if all the required inputs are specified appropriately (e.g., arguments for the function `GridToUTM(ptc, asc)` and Section 5). The following algorithm outlines the **NetworkDistances** procedure and explains the code's major functions; we recommend that users follow along in the `NetworkDistances.R` code (Listing 1, Appendix).

This algorithm is run for each `y` replicate iteration in `newNreps` as follows:

1. Convert **RAMAS** spatial output for patches from grid locations to UTM (m).

`GridToUTM(ptc, asc)` Retrieve spatial data for each patch from **RA-**

MAS output files: `ptcfile` (i.e., `ptc.y.ptc`); and `OrigPatchmap` (i.e., `spp_PA.asc`), where `spp` is typically the species name. The `ptcfile` file indicates patch centers relative to the upper-left corner of the grid (in km), while `OrigPatchmap` georeferences the lower-left corner of the grid (m).⁴ Patch locations are converted to UTM (m) using the geographic information in the `OrigPatchmap` file header. The arguments `ptc` and `asc` reference the `ptcfile` and `OrigPatchmap` files, respectively. The function returns a list with two elements: the location of patches in UTM (m), `patchesUTM`, as an `EventData` object; and the grid outer extent in UTM (m), `gridExtent`.

2. Step 2 is done once if there is only one network, or iteratively if there are multiple sub-networks. First, import the network shapefiles in UTM (m) as a `PolySet` object, `netVect`, which indicates node locations (X, Y), and node connectivity. Set `patchesUTM` to `patches`; this is required because `patches` will be subset during the following calculations to include only the patches within the current network. Each time the loop is iterated, `patchesUTM` is re-set to `patches`, which ensures that all of the patches are considered.
 - (a) If available, load the saved `netVect.RData` object, and skip to Step 2b. Otherwise, proceed as follows:

`CreateUniqueID(dat)` Create a unique ID number for each unique node (X, Y) to ensure the `graph` object is continuous. By default, shapefiles have a different ID for each node, which can cause problems for nodes that are common to two lines that merge into a single stem (e.g., river confluence). These two nodes, which have identical (X, Y) location, must have identical IDs for the `graph` object to consider them attached. The argument `dat` is the network object, and the function returns the updated network object, `netVect` with new columns (especially, `UniqueID`).

`GetToFromDist(dat)` Create a matrix indicating the unique ID for each segment's *start* (e.g., from) and *end* (e.g., to) nodes, as well as the Euclidean distance along each edge. For these short edges, the Euclidean distance sufficiently approximates reality if maps have a fine spatial resolution. Nodes correspond to network vertices, and edges correspond to lines between vertices. Note that the words *to* and *from* simply indicate endpoints because the graph object is *undirected*, meaning that the

⁴Pairwise distances among patches can be calculated from one edge to the other, from the edge of one patch to the center of the other, or from center to center. The center-to-center distance may be very different from the edge-to-edge distance when patches are large (i.e., patch edges extend away from the patch center along network lines). For simplicity, we assume that the distance between patch centers best describes pairwise distances. Thus, network-wise distances are calculated from center-to-center; set `distance <- "Default: Center to center"` in **GRIP2** prior to running iterations to ensure that the `ptfile` file refers to patch centers.

distance from *Pop 1* to *Pop 2* is equal to the distance from *Pop 2* to *Pop 1*. Species that require a *directed* graph (i.e., dispersal depends on direction) will require the user to modify this function. The argument **dat** is the network object, and the function returns **toFromDist** (later renamed **tfTable**), a matrix of node IDs, node locations, and distances between nodes (i.e., edge weights).

Save the output (e.g., network object, **netVect**, and to-from matrix, **tfTable**) as a **netVect.RData** object to be used in subsequent iterations.

(b) Load the saved **netVect.RData** object, then:

EnsureUniqueSites(dat) Ensure that each patch has a unique ID so that pairwise distances are calculated for each patch. Duplicate names are made unique by appending letters (e.g., “a”) to the second duplicate, and so on.⁵ The argument **dat** is the patches, and the function updates the column **Site** with new IDs if duplicates exist.

SnapToNodes(pops) Snap each patch to the nearest network node. Basically, identify the closest node to the patch center, and change the node ID to the patch ID (Figure 4). Thus, patch locations are shifted, but are likely within tolerance considering that **RAMAS** uses a grid to define patches. The search radius is controlled by the parameter **maxD**, which restricts candidate nodes to those within **maxD** units of the patch. It is important to note that patches that are more than **maxD** from all nodes are omitted from the analysis. Although a habitat mask will ensure that patches are located near network lines, distances between patch centers and network nodes can be large when network lines are straight (i.e., fewer nodes), or when patches are large. An iterative search reduces processing time: first search for nodes within $\frac{maxD}{4}$ units of the patch; if there are no nodes, search again within **maxD** units. The argument **pops** is set to the patch. The function returns **minDists**, which indicates the distance from each patch to the nearest node (or **NA** if there are no nodes), and the function updates the node ID in **tfTable** (for both **to** and **from** nodes).

ftM2graphNEL(ft, edgemode, W) This function is from the **graph** package, and creates an object of class **graph** to represent the network. Prior to calling this function, duplicate rows must be omitted from the **tfTable** object. The argument **ft** is the to-from table, **tfTable**, **edgemode** indicates that the **graph** is not directed, and **W** indicates the edge weights. The function returns the **graph** object, **netGraph**.

CalcDistMatrix(dat) Calculate the shortest (e.g., least-cost) network-wise distances (**m**) between each pair of patches in the network using Dijkstra’s (1959) algorithm, implemented by the function **sp.between()**.

⁵Although patches will have unique IDs if **NetworkDistances** is sourced via **GRIP2**, there may be duplicate patch IDs if **NetworkDistances** is run independently.

This function can use parallel processing to decrease processing time, if `doSnow` is `TRUE` (Section 5). Note that the distance from the patch to the network, `minDists`, is not included in the pairwise distance calculation because the patch is technically *on* the network, even if the patch's center is shifted slightly. The argument `dat` is the `graph` object, and the function returns `distMat`, a matrix of pairwise distances with row and column names corresponding to patch names. The `distMat` object is saved as a `distMat.netVect.RData` object in the folder `RDataOutTemp/` so that distances between points in independent sub-networks can be brought together as one large distance matrix using `CombineDistances(dat)` in Step 3.

3. Combine the pairwise distance matrices from each independent sub-network into one large matrix.

`RemoveDupPatches(mat)` Ensure that each patch is only in one network, and ignore networks that do not contain any patches. This function ensures that each patch is snapped to the network with the single closest node. For example, large `maxD` values can cause patches to be inadvertently snapped to two networks if patches are located within `maxD` of nodes on both networks. The argument `mat` is the matrix of `minDists`, named `minDistMat`, which has a column for each network, and a row for each patch. The function returns `patchNetwork`, with a column for each network that contains patches, and a row for each patch that has been snapped to a network (patches are assumed to belong in the network with the nearest node).

`CombineDistances(dat)` Combine distance matrices from each sub-network into one large pairwise distance matrix. The argument `dat` is the set of network name(s) that contain patches, and the function returns the matrix of pairwise distances for the entire group of networks, `pairDists`. The distance between points in different independent sub-networks (i.e., unconnected patches) is `NA`.

`FillPairDists(mat)` Ensure that `pairDists` has one column and one row for each patch, even if the patch was omitted from the analysis. The argument `mat` is `pairDists`, and the function returns an updated `pairDists`.

The `pairDists` matrix is ordered by row and column names for compatibility with **GRIP2** requirements. The matrix is saved as `pairDists.y.RData` in the folder `RDataOutDist/` to be retrieved by **GRIP2** for further analysis.

4. Step 4 is done after **GRIP2** has run to completion, and generates figures of networks and patches. These plots can take considerable time to create when there are many large networks and many iterations; skip this step to speed up the analysis (Section 5).

PlotNetworkPatches() Plot georeferenced network(s) and patches in UTM (m). There are no arguments, and the function does not return anything; instead, the function creates a portable document format (PDF) file in the folder **RDataOutDist/** named **plot.pdf**, with one page for each iteration (Figure 5). Patch names in green have been snapped to network lines; patch names in red have been omitted from the analysis (i.e., patches more than **maxD** units from all network nodes).

5 INCORPORATING NetworkDistances INTO GRIP2

In addition to the usual controls and parameters required for **GRIP2** and **RAMAS**, **NetworkDistances** requires several additional user-specified inputs which must be specified in **GRIP2** or at the start of the **NetworkDistances** code:

calc_network_dist Set to **TRUE** to calculate distances along networks; set to **FALSE** to calculate Euclidean distances. Value: logical.

maxD Maximum distance (m) from each patch to search for candidate network nodes in **SnapToNodes(pops)**. Value: number.

doSnow Set to **TRUE** to use parallel processing in **CalcDistMatrix(dat)**; set to **FALSE** for no parallel processing. Value: logical.

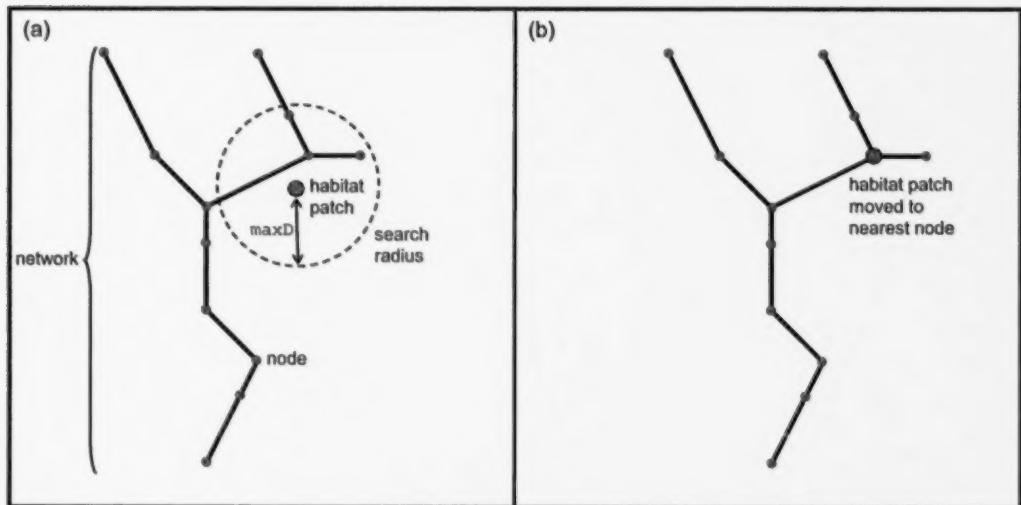


Figure 4. Hypothetical network and habitat patch (a). The network is composed of nodes connected by segments. Three nodes are within **maxD** units of the patch's center; the **SnapToNodes(pops)** function shifts the patch's location to the nearest node (b).

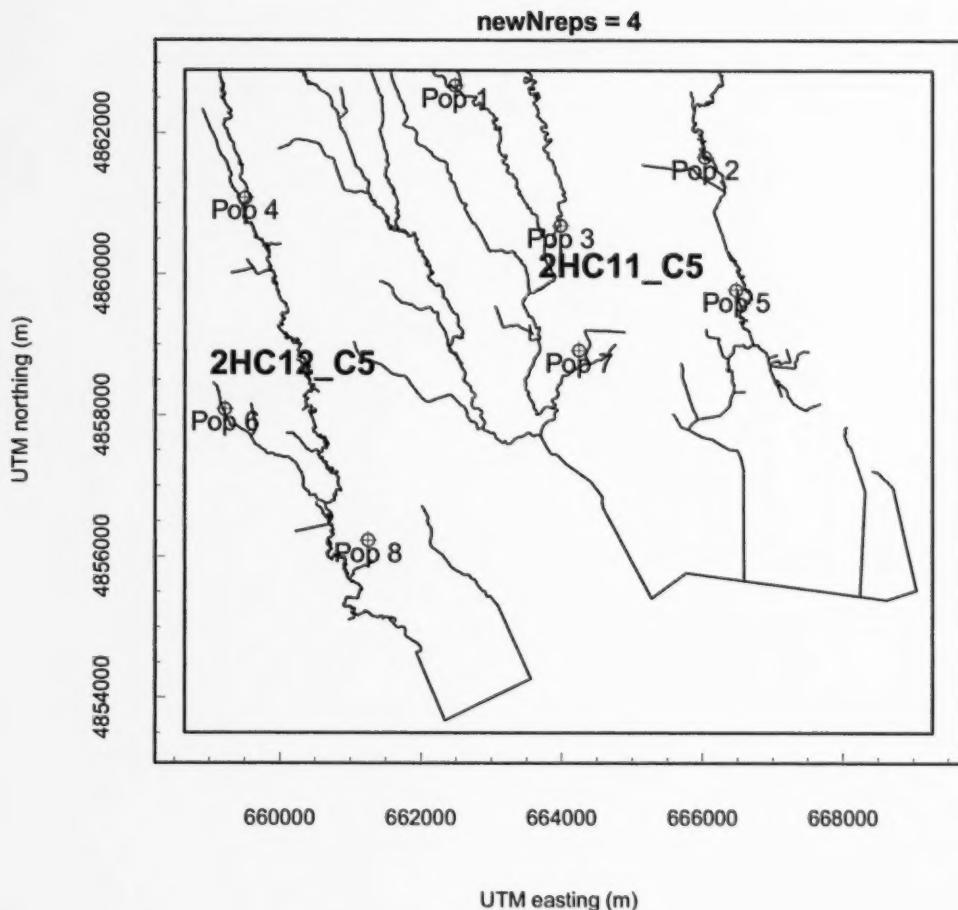


Figure 5. Plot created by the function `PlotNetworkPatches()` showing the eight habitat patches and two networks on the fourth iteration of the redside dace study area. Note that patches `Pop_4`, `Pop_6`, and `Pop_8` are all connected, and are on network `2HC12_C5`; these patches are not connected to the patches on network `2HC11_C5` (e.g., `Pop_1`). Note also that patch names are shown in black for printing purposes, but would normally be shown in green (i.e., they have all been snapped to network lines).

cType Cluster type (if `doSnow`). Use “`SOCK`” for Windows machines, or either “`SOCK`” or “`MPI`” for non-Windows machines. Value: character.

nCores Number of cores for parallel processing (if `doSnow`). For example, in Windows, this indicates the number of instances of `Rscript.exe` that are initialized and used in `CalcDistMatrix(dat)`. Note that `nCores` controls a trade-off between the number of cores, and the memory available to each core. Value: integer.

coreName Processor name (if `doSnow`). Value: character (e.g., “localhost”).

nZone UTM zone, required to align patches and network lines. Value: integer.

doSpatPlots Set to `TRUE` to call `PlotNetworkPatches()` and generate figures showing patches and networks for each iteration; set to `FALSE` to skip this step. Value: logical.

networks Shapefile network name(s), not including extension(s). If there are multiple shapefiles (i.e., the network is broken up into independent sub-networks), **networks** is a concatenation of each sub-network name; if there is only one network, **networks** is the network name. Input shapefiles (in UTM, m) must be in the folder `NetworkShapefiles/`. Value: character vector (e.g., `c("2HC09", "2HC10")` for multiple sub-networks; character (e.g., “`2A11`”) for one network).

The **NetworkDistances** code should be in the same folder as **GRIP2**, the *working directory*. Create two folders in the working directory: `NetworkShapefiles/`, and `SavedNetworkObjects/`. The folder `NetworkShapefiles/` contains the shapefiles for the network(s). The folder `SavedNetworkObjects/` may contain saved `netVect.RData` objects from previous iterations to speed up computations, if they are available (Sub-section 4.2, Step 2a).

Two additional folders are created during the simulation: `RDataOutTemp/`, and `RDataOutDist/`. The folder `RDataOutTemp/` holds temporary **R** output each iteration. The folder `RDataOutDist/` contains pairwise distance matrices for each iteration and network. Pairwise distance objects are named `pairDists.y.RData` in order to be retrieved later by **GRIP2** to calculate various statistics. Two other objects are saved in the folder `RDataOutDist/` under the names `patchNetworkDist.y.RData` (contains `minDistMat` and `patchNetwork`), and `patches.y.RData` (contains `patches` and `patchesUTM`). This folder may also contain the figure of patches and network lines, `plot.pdf`.

5.1 DISTANCE UNITS AND CONVERSIONS

Distance units may vary between the **RAMAS** programme, the **GRIP2** script, and the **NetworkDistances** code. For consistency, the **NetworkDistances** code uses metres (converting kilometres to metres when necessary). For the RSD analysis, network shapefiles are in metres, and **RAMAS** output files are in metres (e.g., `Patchmap`) and kilometres (e.g., `ptcfile`). **NetworkDistances** calculations and inputs (e.g., `maxD`) are in metres. However, because **RAMAS** input files require distances in kilometres, `pairDists` is converted from metres to kilometres just prior to being returned to **GRIP2** as a matrix of pairwise distances, `Pairwise_Distance`. It is critical that users ensure that distances have expected units in **RAMAS**, **GRIP2**, and **NetworkDistances** input and output files.

6 VERIFYING NetworkDistances AND EXTENSIONS

Distances calculated using the `NetworkDistances` code should sufficiently approximate reality if network shapefiles are accurate and of sufficient spatial resolution. However, we recommend that users confirm the accuracy of the `NetworkDistances` output by checking various statistics, the distance matrix `pairDists`, and the figure generated by the function `PlotNetworkPatches()`. Additionally, ensure that **RAMAS** output files (i.e., `spp.asc`) line up with networks by plotting patches and network lines, as well as verifying the patch map grid location (Subsection 4.2, Step 1). Ensure that `maxD` is sufficiently large to locate candidate nodes in `SnapToNodes(pops)`. Investigate the matrices in `patchNetworkDist.y.RData` to ensure that patches are assigned to the correct network. These matrices will also indicate whether `maxD` is too small (e.g., patches are omitted), or too large (e.g., snapped distances are much shorter than `maxD`). Also, ensure that **RAMAS** files, grids, and network lines have identical projections and correct units.

As previously mentioned, one extension is to use directed graphs; for example, migration distance may depend on direction for fish that inhabit fast-flowing rivers (Step 2a). A second use of directed graphs is to model the effects of patch size (e.g., area) and population on migration; for example, large patches may have more immigrants, while large populations may have more emigrants. Another extension is to incorporate a changing spatial network over time. For example, a previously continuous river network could become fragmented by dams. This type of temporal change would increase processing time because year-specific network objects would have to be calculated each year.

7 ACKNOWLEDGEMENTS

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APPENDIX

Electronic copies of the modified **GRIP2** script for use with **NetworkDistances**, the **NetworkDistances.R** code (Listing 1), and the RSD study area data (e.g., river networks, RSD habitat map) are available free from the authors.

Listing 1. The **NetworkDistances** code (**NetworkDistances.R** version 1.0) is written in the programming language **R** (RDCT 2011).

```
1 #####  
2 #  
3 # Author: Matthew H. Grinnell  
4 # Affiliation: Pacific Biological Station, Fisheries and Oceans Canada  
5 # Research group: Conservation Biology Section (Janelle M. R. Curtis)  
6 # Contact: e-mail: matt.grinnell@dfo-mpo.gc.ca | tel: (250)756.7326  
7 # e-mail: janelle.curtis@dfo-mpo.gc.ca | tel: (250)756.7157  
8 # Project: GRIP2 extension for movement between patches within networks  
9 # Code name: NetworkDistances.R  
10 # Code version: 1.0  
11 # Date started: 2010-11-30  
12 # Date modified: 2011-11-16  
13 #  
14 # Goal: Convert spatial lines (i.e., networks) and points (i.e., patches) to a  
15 # graph object, and calculate network-wise distances between each pair of  
16 # habitat patches. Output a matrix of pairwise distances, pairDists, which  
17 # is also saved as a .RData object in the folder RDataOutDist. These objects  
18 # are indexed by iteration number y in newNreps (e.g., pairDists.i.RData).  
19 #  
20 # Requirements: This code is designed for use with GRIP[1], and RAMAS GIS  
21 # 5.0[2]; however, the code could be modified for stand-alone use. Regardless  
22 # of whether NetworkDistances is used alone or with GRIP2, read the  
23 # NetworkDistances user manual[3] for additional details.  
24 #  
25 # Notes: Please contact the authors if you have suggestions, comments, or  
26 # concerns. Additionally, we are attempting to keep track of this code's use;  
27 # please contact the authors if the code was useful for research. We recommend  
28 # that users verify their output by checking various statistics and graphs. We  
29 # assume that the user has a working ability with R[4], and is familiar with  
30 # spatial data. It is crucial that users verify that distances are in the  
31 # correct units throughout this script! This code comes with absolutely no  
32 # warranty.  
33 #  
34 # References:  
35 # [1] Curtis, J. M. R. and Naujokaitis-Lewis, I. R. 2008. Source code for the  
36 # program GRIP 1.0 (Generation of Random Input Parameters).  
37 # URL http://esapubs.org/archive/app1/A018/033/suppl-1.htm. Ecological  
38 # Archives: A018-033-S1 (Supplement)  
39 # [2] Akcakaya, H. R. 2005. RAMAS GIS: Linking spatial data with population  
40 # viability analysis. Applied Biomathematics. URL www.ramas.com. User  
41 # manual for version 5  
42 # [3] Grinnell, M. H. and Curtis, J. M. R. 2011. User manual for  
43 # NetworkDistances 1.0: Calculating network-wise distances between habitat  
44 # patches for spatially restricted species. Can. Tech. Rep. Fish. Aquat.  
45 # Sci. 2960: iv + 29 p.  
46 # [4] RDCT (R Development Core Team). 2011. R: A language and environment for  
47 # statistical computing. URL www.R-project.org. R foundation for  
48 # Statistical Computing. Vienna, Austria. R version 2.13.0  
49 #  
50 #####  
51 ##### Start file 'NetworkDistances.R' #####  
52 #####
```

```

55
56 # Ensure that all the required user-specified inputs are present. Note: if
57 # NetworkDistances is not called from GRIP2, these parameter values need to be
58 # initialized prior to here. Also, ensure the proper file structure has been
59 # created, the required habitat patch information is available (i.e., the ptc
60 # and asc arguments to the function GridToUTM), and define y.
61 if( !all(exists(x=c("maxD", "doSnow", "cType", "nCores", "coreName", "nZone",
62   "doSpatPlots", "networks")))) {
63   # Stop everything
64   stop( "Missing required user-specified inputs for 'NetworkDistances.R'" )
65 } # End ensure user-inputs

66 # Create a temporary directory to hold output each iteration
67 if( "RDataOutTemp" %in% list.files( ) ) {
68   # Delete the old directory
69   unlink( x="RDataOutTemp", recursive=TRUE )
70   # Create a new directory
71   dir.create( path="RDataOutTemp" )
72   # End if directory exists, otherwise
73 } else {
74   # Make a new directory
75   dir.create( path="RDataOutTemp" )
76 } # End if the directory does not exist

77 # Get habitat patch locations (referenced via the grid) from the .ptc file, and
78 # grid georeference info from the .asc file (to georeference the patches).
79 # Convert to UTM and return habitat patches: patchesUTM. Note that users *must*
80 # verify that this function specifies distance units correctly: as is, this
81 # function expects distances in m (asc) and km (ptc), and converts to m.
82 GridToUTM <- function( ptc, asc ) {
83   # Get the first item from the first nmax lines in the ptc file
84   firstItemPTC <- scan( file=ptc, skip=0, sep=",", what="character",
85     quiet=TRUE, flush=TRUE, blank.lines.skip=FALSE, nmax=200 )
86   # Get line info for the habitat patch data (usually line 88)
87   linePatchPTC <- grep( pattern=paste(Npops, "populations", sep=" "),
88     x=firstItemPTC, perl=TRUE )[1]
89   # If linePatchPTC is NA (possibly due to not enough lines), search again
90   if( is.na(linePatchPTC) ) {
91     # Get the first item from all the lines in the ptc file: this can take
92     # a long time
93     firstItemPTC <- scan( file=ptc, skip=0, sep=",", what="character",
94       quiet=TRUE, flush=TRUE, blank.lines.skip=FALSE )
95     # Get line info for the habitat patch data
96     linePatchPTC <- grep( pattern=paste(Npops, "populations", sep=" "),
97       x=firstItemPTC, perl=TRUE )[1]
98     # Print a warning
99     warning( "Increase 'nmax' in firstItemPTC() to avoid scanning whole file" )
100   } # End if linePatchPTC is NA
101   # If linePatchPTC is *still* NA, error
102   if( is.na(linePatchPTC) ) {
103     # Error message
104     stop( "Check file '", ptc, "' unable to find patch info" )
105   } # End if linePatchPTC is *still* NA
106   # Scan to get patch info into a list: Site, X, and Y (in km, referenced via
107   # the grid)
108   patchData <- scan( file=ptc, skip=linePatchPTC, nlines=Npops, sep=",",
109     what=list(Site="", X=0, Y=0), quiet=TRUE, flush=TRUE )
110   # Get the first item from the first nmax lines in the (sometimes large) .asc
111   # file. This *should* contain the required lines, since they are usually at
112   # the top of the .asc file (as a header).
113   firstItemASC <- scan( file=asc, skip=0, sep="\t", what="character",
114     quiet=TRUE, flush=TRUE, blank.lines.skip=FALSE, nmax=10 )
115   # Get the line info for the X location
116   lineXASC <- grep( pattern="xllcorner", x=firstItemASC, perl=TRUE )[1]
117   # If lineXASC is NA (possibly due to not enough lines), search again
118

```

```

121 if( is.na(lineXASC) ) {
122   # Get the first item from all lines in the asc file -- this can take
123   # much longer!
124   firstItemASC <- scan( file=asc, skip=0, sep="\t", what="character",
125     quiet=TRUE, flush=TRUE, blank.lines.skip=FALSE )
126   # Get the line info for the X location
127   lineXASC <- grep( pattern="xllcorner", x=firstItemASC, perl=TRUE )[1]
128   # Print a warning
129   warning( "Increase 'nmax' in firstItemASC() to avoid scanning whole file" )
130 } # End if lineXASC is NA
131 # If lineXASC is *still* NA, error
132 if( is.na(lineXASC) ) {
133   # Error message
134   stop( "Check file '', asc, ''; unable to georeference the grid" )
135 } # End if lineXASC is *still* NA
136 # Georeference the grid's location: get the left side 'X' location (UTM, m)
137 ASCgridLLX <- as.numeric( scan(file=asc, skip=lineXASC - 1, sep="\t",
138   what=list(NULL, "numeric"), quiet=TRUE, flush=TRUE, nlines=1)[[2]] )
139 # Get the line info for the Y location
140 lineYASC <- grep( pattern="yllcorner", x=firstItemASC, perl=TRUE )[1]
141 # Georeference the grid's location: get the lower 'Y' location (UTM, m)
142 ASCgridLLY <- as.numeric( scan(file=asc, skip=lineYASC - 1, sep="\t",
143   what=list(NULL, "numeric"), quiet=TRUE, flush=TRUE, nlines=1)[[2]] )
144 # Get the line info for the cell size
145 lineCellASC <- grep( pattern="cellsize", x=firstItemASC, perl=TRUE )[1]
146 # Get the grid cell size (m)
147 ASCgridSize <- as.numeric( scan(file=asc, skip=lineCellASC - 1, sep="\t",
148   what=list(NULL, "numeric"), quiet=TRUE, flush=TRUE, nlines=1)[[2]] )
149 # Get the line info for the number of rows
150 lineRowsASC <- grep( pattern="nrows", x=firstItemASC, perl=TRUE )[1]
151 # Get the number of rows
152 ASCgridRows <- as.numeric( scan(file=asc, skip=lineRowsASC - 1, sep="\t",
153   what=list(NULL, "numeric"), quiet=TRUE, flush=TRUE, nlines=1)[[2]] )
154 # Get the line info for the number of columns
155 lineColsASC <- grep( pattern="ncols", x=firstItemASC, perl=TRUE )[1]
156 # Get the number of columns (grid X dimension)
157 ASCgridCols <- as.numeric( scan(file=asc, skip=lineColsASC - 1, sep="\t",
158   what=list(NULL, "numeric"), quiet=TRUE, flush=TRUE, nlines=1)[[2]] )
159 # If any of lineYASC, lineCellASC, lineRowsASC, or lineColsASC is NA, error
160 if( is.na(lineYASC) | is.na(lineCellASC) | is.na(lineRowsASC) |
161   is.na(lineColsASC) ) {
162   # Error message
163   stop( "Check file '', asc, ''; unable to georeference the grid (2)" )
164 } # End if any of lineYASC, lineCellASC, lineRowsASC, or lineColsASC is NA
165 # Put scanned data into a dataframe with columns EID, X (convert km to m),
166 # Y (convert km to m), and Site. Note that users *must* verify that this
167 # function specifies distance units correctly
168 patchDF <- data.frame( EID=1:Nops, X=patchData$X*1000, Y=patchData$Y*1000,
169   Site=patchData$Site )
170 # Find the top of the grid (UTM, m)
171 gridTop <- ASCgridRows * ( ASCgridRows * ASCgridSize )
172 # Find the right side of the grid (UTM, m)
173 gridRight <- ASCgridLLX + ( ASCgridCols * ASCgridSize )
174 # Convert patch (X, Y) locations from grid to UTM (m; currently, (X, Y)
175 # indicates the number of grid cells from the upper-left corner of the grid)
176 patchDF$X <- ASCgridLLX + patchDF$X
177 patchDF$Y <- gridTop - patchDF$Y
178 # Convert to EventData (georeferenced in UTM, m for PBSmapping)
179 patchEvent <- as.EventData( x=patchDF, projection="UTM", zone=nZone )
180 # Set up a list to return
181 res <- list( patchEvent=patchEvent,
182   extent=list( top=gridTop, bottom=ASCgridLLY, left=ASCgridLLX,
183     right=gridRight ) )
184 # Return the list (habitat patches (as EventData) and grid extent)
185 return( res )

```

```

185 } # End GridtoUTM function

187 # Run the GridToUTM function to get the patches and grid extent
188 getGridToUTM <- GridToUTM( ptc=ptcfile, asc=OrigPatchmap )
189
190 # Get the patches
191 patchesUTM <- getGridToUTM$patchEvent
192
193 # Get the grid extent (for the plot below)
194 gridExtent <- getGridToUTM$extent
195
196 # Loop over the number of networks
197 for( i in 1:length(networks) ) {
198
199     # Get the river network (via watershed name). Note that users *must* verify
200     # that this function specifies distance units correctly: as is, this function
201     # expects distances in m.
202     netVect <- importShapefile( readDBF=TRUE, projection="UTM", zone=nZone,
203         fn=paste("NetworkShapefiles/", networks[i], ".shp", sep="") )
204
205     # Select only the required columns (to reduce object size)
206     netVect <- subset( netVect, select=c(PID, SID, POS, X, Y) )
207
208     # Get the original river points
209     patches <- patchesUTM
210
211     # If the saved data object from a previous simulation is NOT available in the
212     # working directory, run the entire analysis (this may take some time) and
213     # save the required object for the next simulation
214     if( !paste(networks[i], ".RData", sep="") %in%
215         list.files("SavedNetworkObjects") ) {
216
217         # Create a column to indicate the unique ID for each unique node. Note that
218         # some nodes are repeated (i.e., the bottom coordinates of two streams that
219         # merge (i.e., become one large stream) will be the same as the top
220         # coordinates of the stream that they merge into). These nodes need to have
221         # the same ID numbers for the graph object to consider them the same (which
222         # they are).
223         CreateUniqueID <- function( dat ) {
224
225             # Select the columns of XY data from the data.frame and load as a matrix
226             mat <- matrix( cbind(dat$X, dat$Y), nrow=nrow(dat), ncol=2 )
227
228             # Initialize a vector to hold unique IDs
229             vec <- 0
230
231             # Fill vec with consecutive numbers for non-duplicated rows
232             vec[!duplicated(mat)] <- 1:nrow( mat[!duplicated(mat), ] )
233
234             # Get unique duplicated rows
235             dups <- unique( mat[duplicated(mat), ] )
236
237             # Loop over unique duplicated rows
238             for( i in 1:nrow(dups) ) {
239
240                 # Determine the indices in mat that match the ith duplicated row
241                 iInd <- mat[ ,1] == dups[i, 1] & mat[ ,2] == dups[i, 2]
242
243                 # Set duplicate rows to the first number (the ID)
244                 vec[iInd] <- vec[iInd][1]
245
246             } # End loop over unique dups
247
248             # Add the data to dat, and initialize columns for site name and distance
249             dat$UniqueID <- vec
250             dat$SiteName <- NA
251             dat$dist <- NA
252
253             # Return the site locations
254             return( dat )
255         } # End CreateUniqueID function
256         netVect <- CreateUniqueID( dat=netVect )
257
258         # Collect garbage
259         gc()
260
261         # Get locations "to" and "from", as well as distances between location
262         # pairs
263     }

```

```

251 GetToFromDist <- function( dat ) {
252   mat <- matrix( NA, nrow=nrow(dat), ncol=7 )
253   colnames( mat ) <- c( "frID", "toID", "frX", "frY", "toX", "toY",
254     "dist" )
255   count <- 0 # Initialize counter (for rows)
256   # Pull required columns into a matrix
257   dat <- as.matrix( dat[, 1:6], ncol=6, byrow=TRUE )
258   # Loop over PIDs
259   for( i in 1:length(unique(dat[, "PID"])) ) {
260     datPID <- subset( dat, dat[, "PID"] == unique(dat[, "PID"])[i] )
261     # Loop over SIDs within PIDs
262     for( j in 1:length(unique(datPID[, "SID"])) ) {
263       datSID <- subset( datPID,
264         datPID[, "SID"] == unique(datPID[, "SID"])[j] )
265       # Loop over rows within SIDs within PIDs
266       for( k in 1:(nrow(datSID)-1) ) {
267         # Update the counter for new row
268         count <- count + 1
269         # Get coordinates
270         mat[count, "frX"] <- datSID[k, "X"]
271         mat[count, "frY"] <- datSID[k, "Y"]
272         mat[count, "toX"] <- datSID[(k+1), "X"]
273         mat[count, "toY"] <- datSID[(k+1), "Y"]
274         # Get the UniqueID (i.e., the river node numbers)
275         mat[count, "frID"] <- datSID[k, "UniqueID"]
276         mat[count, "toID"] <- datSID[(k+1), "UniqueID"]
277         # Calculate the distance
278         mat[count, "dist"] <- sqrt( (datSID[k, "X"] - datSID[(k+1), "X"])^2
279           + (datSID[k, "Y"] - datSID[(k+1), "Y"])^2 )
280       } # End loop over rows within SID within PID
281     } # End loop over SID within PID
282     # Remove rows that are NA (these are due to repeated points)
283     return( na.omit(mat) )
284   } # End GetToFromDist function
285   toFromDist <- GetToFromDist( dat=netVect )
286   # Collect garbage
287   gc()
288   # Change the class of the toFromDist to a data.frame to allow factors for
289   # node names (population sampling points)
290   tfTable <- data.frame( frID=toFromDist[, "frID"],
291     toID=toFromDist[, "toID"], frX=toFromDist[, "frX"],
292     frY=toFromDist[, "frY"], toX=toFromDist[, "toX"],
293     toY=toFromDist[, "toY"], dist=toFromDist[, "dist"] )
294   # Remove toFromDist to save memory (this can be a large object)
295   rm( toFromDist )
296   # Save the required objects for the next simulation
297   save( list=c("netVect", "tfTable"),
298     file=paste("SavedNetworkObjects/", networks[i], ".RData", sep="") )
299   } # End if the saved object is not present in the working directory
300
301   # If the saved data object from a previous simulation IS available, load the
302   # saved object to reduce computation time if desired
303   if( paste(networks[i], ".RData", sep="") %in% 
304     list.files("SavedNetworkObjects") ) {
305     # Load the object
306     load( file=paste("SavedNetworkObjects/", networks[i], ".RData", sep="") )
307     # Ensure that site names and distances from the last iteration are NA
308     netVect$SiteName <- NA
309     netVect$DistToSite <- NA
310   } # End if using saved object
311
312   # Ensure that all sampling points have unique IDs
313   EnsureUniqueSites <- function( dat ) {
314     # Letter index for first site

```

```

315  iLet <- 0
316  # Get the original site names
317  sites <- as.character( dat$Site )
318  # Print a warning that site(s) have been renamed
319  warning( "Duplicate site name(s) were renamed (", networks[i]," )")
320  # Iterative rename function
321  RenameRename <- function( siteNames ) {
322      # Index the duplicated sites
323      ind <- duplicated( siteNames )
324      # Rename the sites
325      siteNames[ind] <- paste( siteNames[ind], letters[iLet], sep="" )
326      return( siteNames )
327  } # End RenameRename function
328  # Send the site names to the RenameRename function while there are
329  # duplicates
330  while( TRUE %in% duplicated(sites) ) {
331      # Update the counter for new letters
332      iLet <- iLet + 1
333      # Rename sites
334      sites <- RenameRename( siteNames=sites )
335  } # End while loop
336  # Return the new site names as factors
337  return( as.factor(sites) )
338 } # End CreateUniqueID function
339
340 # If there are duplicate site names, rename them
341 if( TRUE %in% duplicated(patches$Site) ){
342     patches$Site <- EnsureUniqueSites( dat=patches )
343 } # End if duplicate rows
344
345 # Collect garbage
346 gc( )
347
348 # Add the sampling points to the to-from matrix at the nearest node, within
349 # maxD units. Outputs the minimum distances for each population, and updates
350 # the nodes that are now population points. If no nodes are within maxD units
351 # of the point, the output is NA, and the point is ignored.
352 SnapToNodes <- function( pops ) {
353     # Coordinates
354     pt <- c( as.numeric(pops["X"]), as.numeric(pops["Y"]) )
355     # Function to get the set of nodes within some proportion of maxD units
356     # from pt. Returns a subset of netVect that is within the specified
357     # distance (up to a maximum of maxD).
358     GetPoints <- function( srchD ) {
359         # Get outer range in X
360         xs <- c( pt[1] - srchD, pt[1] + srchD )
361         # Get outer range in Y
362         ys <- c( pt[2] - srchD, pt[2] + srchD )
363         # Select the river nodes within the outer range to limit the search
364         subRiv <- netVect[ netVect$X>xs[1] & netVect$X<xs[2] & netVect$Y>ys[1] &
365             netVect$Y<ys[2], ]
366         # Return the subset of netVect
367         return( subRiv )
368     } # End GetPoints function
369     # Run the GetPoints function with maxD/4
370     iNodes <- GetPoints( srchD=maxD/4 )
371     # If there are no nodes, run GetPoints again with maxD
372     if( dim(iNodes)[1] == 0 ) iNodes <- GetPoints( srchD=maxD )
373     # Set up a temporary vector to hold distances
374     dVec <- 0.
375     # Continue only if there are elements to iNodes
376     if( dim(iNodes)[1] >= 1 ) {
377         # Loop over nodes and calculate Euclidian distance
378         for( i in 1:nrow(iNodes) ) {
379             dVec[i] <- sqrt( (pt[1] - iNodes$X[i])^2 + (pt[2] - iNodes$Y[i])^2 )

```

```

} # End loop over rows in nodes
381 # Ensure that the minimum distance is <= maxD (note that this might not
382 # be true because dVec's are for points within the box, but we need to
383 # ensure that the radius is <= maxD
384 if( min(dVec) <= maxD ) {
385     # Determine the position of the closest (select only one if a tie)
386     iRow <- which(min(dVec) == dVec)[1]
387     # Get its unique ID
388     iID <- iNodes$UniqueID[iRow]
389     # Determine whether the node is already a site. This can occur if two
390     # sampling locations are close together, and snap to the same node.
391     # Note that iID is a single number, but may reference multiple nodes;
392     # for example, the node is a junction (i.e., location at which two
393     # streams merge)
394     # If the node is not already a site:
395     if( is.na(netVect$SiteName[netVect$UniqueID == iID])[1] ) {
396         # Update the node to reflect that it's a sampling location (from)
397         tfTable$frID[tfTable$frID == iID] <- pops["Site"]
398         # Update the node to reflect that it's a sampling location (to)
399         tfTable$toID[tfTable$toID == iID] <- pops["Site"]
400         # Also, update netVect to indicate population site and distance to
401         # node
402         netVect$SiteName[netVect$UniqueID == iID] <- pops["Site"]
403         netVect$DistToSite[netVect$UniqueID == iID] <- min( dVec )
404     } # End if the node is not already a site
405     # If the node is already a site:
406     else {
407         # Get the old site name
408         oldName <- netVect$SiteName[netVect$UniqueID == iID][1]
409         oldXY <- c( netVect$X[netVect$UniqueID == iID][1],
410                   netVect$Y[netVect$UniqueID == iID][1] )
411         # Make a new row to add to the dataframe, with the distance between
412         # the new and old sites equal to zero (i.e., same node/location)
413         newRow <- tfTable[1, ]
414         newRow$frID <- pops["Site"]
415         newRow$toID <- oldName
416         newRow$frX <- oldXY[1]
417         newRow$frY <- oldXY[2]
418         newRow$toX <- oldXY[1]
419         newRow$toY <- oldXY[2]
420         newRow$dist <- 0.
421         # Finally, append the new rows to the to-from matrix
422         tfTable <- rbind( tfTable, newRow )
423         # Also, update netVect to indicate that the node has two population
424         # sites and the max of the distances
425         netVect$SiteName[netVect$UniqueID == iID] <-
426             paste( netVect$SiteName[netVect$UniqueID == iID][1], pops["Site"],
427                   sep=". " )
428         netVect$DistToSite[netVect$UniqueID == iID] <-
429             max(min(dVec), netVect$DistToSite[netVect$UniqueID == iID][1])
430         # Print a warning to indicate the node is already a site
431         warning( "Sites ", pops["Site"], " and ", oldName,
432                  " are on the same node (", networks[i], ")" )
433     } # End if the node is already a site
434 } # End if min(dVec) <= maxD
435 # Otherwise, min(dVec) is > maxD
436 else dVec <- NA
437 } # End if there are rows in iNodes
438 # If there are no nodes, dist is NA, and print a warning
439 if( dim(iNodes)[1] == 0 ) dVec <- NA
440 # Return the distance between the population point and the node
441 return( min(dVec) )
442 } # End SnapToNodes function
443
# Add patches to network

```

```

445 minDists <- apply( X=patches, MARGIN=1, FUN=SnapToNodes )

447 # Append minDists to minDistMat. This will allow the identification of
# patches that occur in multiple networks (i.e., when maxD is too large),
449 # and assign the patch to the network that is closest. If it's the first
# iteration
451 if( i==1 ) {
452   # Set up the empty matrix
453   minDistMat <- matrix(NA, nrow=nrow(patches), ncol=length(networks) )
454   # Name columns as networks
455   colnames( minDistMat ) <- networks
456   # Name rows as patches
457   rownames( minDistMat ) <- patches$Site
458   # Add minDists to the 1st column
459   minDistMat[, 1] <- minDists
460   # End if the 1st iteration
461 } else {
462   # Add minDists to the ith column
463   minDistMat[, i] <- minDists
464 } # End if iteration is 2nd or more

465 # Collect garbage
466 gc( )

467 # Make the graph object. Take in the toFromDist data.frame, and output the
# graph object indicating paths between vertices (some of which are
468 # population sampling points) and distances (calculated as weights in the
# graph object). First, check for and remove edges that are specified
469 # multiple times. To save time, only do this if the network has patches.
470 if( any(patches$Site %in% tfTable$frID) |
471     any(patches$Site %in% tfTable$toID) ) {
472   # Make a graph with all the nodes
473   netGraphAll <- graph.data.frame( tfTable[,1:2], directed=FALSE )
474   # Remove nodes that are duplicated
475   tfTable <- tfTable[!is.multiple( graph=netGraphAll ), ]
476   # Make a graph with unique nodes
477   netGraph <- ftM2graphNEL( ft=cbind(tfTable$toID, tfTable$frID),
478     edgemode="undirected", W=tfTable$dist )
479 } # End if the network has patches

480 # Collect garbage
481 gc( )

482 # Calculate distance matrix between pairs of sampling points. If a pair of
# points are not connected (i.e., not joined by lines), the distance is NA.
# The diagonal is zero (i.e., distance between a point and itself, and the
# distance "to" equals the distance "from" (i.e., direction is irrelevant).
483 CalcDistMatrix <- function( dat ) {
484   # Get character vector of unique site names from the graph object. This is
485   # important because the distance function will work hard to calculate
486   # distances for unconnected patches, which takes a very long time. So,
487   # only include patches that are actually on the graph
488   patchSites <- patches$Site[ which(patches$Site %in% nodes(netGraph)) ]
489   patchSites <- as.character( patchSites )
490   # Set up the empty distance matrix, with site names for rows and cols
491   dMat <- matrix( NA, nrow=length(patchSites), ncol=length(patchSites) )
492   colnames( dMat ) <- patchSites
493   rownames( dMat ) <- patchSites
494   # First, generate a table of indices for the upper triangle of dMat
495   num <- length( patchSites )
496   idx <- expand.grid( i=1:num, j=1:num )[upper.tri( diag(num),
497     diag=FALSE ), ]
498   # Function to get the distance: apply over rows of idx to fill in the upper
499   # triangle of the distance matrix
500   GetDistance <- function( dat, patchSites=patchSites, netGraph=netGraph ) {
501

```

```

# Load the required library
511 require( RBGL )
# Get the pair of point names
513 ptPair <- c( patchSites[dat[1]], patchSites[dat[2]] )
# Determine the shortest route and distance between the pair of points
515 pairDist <- sp.between( g=netGraph, start=ptPair[1], finish=ptPair[2],
    detail=FALSE )
517 # Pull out the distance between the pair
518 return( pairDist[[1]]$length )
519 } # End GetDistance function
# If using only one core (and idx has some data)
521 if( !doSnow & dim(idx)[1] > 0 ) {
    # Apply the indices to the function and output distances
523 dists <- apply( X=idx, MARGIN=1, FUN=GetDistance,
    patchSites=patchSites, netGraph=netGraph )
525 } # End if only one core
# If using multiple cores (and idx has some data)
527 if( doSnow & dim(idx)[1] > 0 ) {
    # Apply the indices to the function and output distances
529 dists <- parApply( cl=snowClust, X=idx, MARGIN=1, FUN=GetDistance,
    patchSites=patchSites, netGraph=netGraph )
531 } # End if using more than one core
# If idx does not have any data
533 if( dim(idx)[1] == 0 ) dists <- NA
# Place distances into the upper triangle
535 dMat[upper.tri(dMat, diag=FALSE)] <- dists
# And the lower triangle
537 dMat[lower.tri(dMat)] <- t(dMat)[lower.tri(dMat)]
# Update the diagonal
539 diag( dMat ) <- 0.
# Return the matrix
541 return( dMat )
} # End CalcDistMatrix function
543
# To save time, calculate distances only if the network has habitat patches
545 if( any(patches$Site %in% tfTable$frID) |
    any(patches$Site %in% tfTable$toID) ) {
    distMat <- CalcDistMatrix( dat=netGraph )
} # End if there are patches
549
# If there aren't any patches, distMat is "empty"
551 if( !any(patches$Site %in% tfTable$frID) &
    !any(patches$Site %in% tfTable$toID) ) {
    distMat <- matrix( NA, nrow=0, ncol=0 )
} # End if there are no patches
555
# Collect garbage
557 gc( )
559
# Save the distance matrix as an .RData object
560 save( distMat,
561     file=paste("RDataOutTemp/distMat.", networks[i], ".RData", sep="") )
563 } # End i loop over the number of networks
565
# Subset minDistMat to only have patches that are in a network, and to only
# have networks that have patches. Also, each patch should only be in one
566 # network, which is the network that had the nearest node. This is to ensure
# that there are no duplicates in pairDists (output from CombineDistances,
569 # below)
RemoveDupPatches <- function( mat ) {
571     # Determine which rows are ALL NA (i.e., patches that were not snapped
# to a node in any networks -- these patches are omitted from the analysis)
572     naRows <- apply( X=mat, MARGIN=1, FUN=function(x) all(is.na(x)) )
# Take the inverse
573

```

```

575 naRows2 <- naRows == FALSE
576 # Select the rows with (patches) that were snapped to node(s)
577 mat2 <- subset( mat, subset=naRows2 )
578 # Loop over rows in mat, and make sure that each patch only "belongs" to
579 # one node (network); if there are two, set the further one to NA to ensure
580 # that the patch is only in one network
581 for( k in 1:nrow(mat2) ) {
582   # Get the elements in row k that are not NA
583   dat <- mat2[k, is.na(mat2[k, ]) == FALSE]
584   # If there are more than one, pick the smallest one. Otherwise, ignore
585   if( length(dat) >= 2 ) {
586     # Get the min
587     minDat <- min( dat )
588     # Set the other(s) in the row to NA
589     mat2[k, which(mat2[k, ] != minDat)] <- NA
590   } # End if more than 2 networks
591 } # End loop over k rows in mat
592 # Determine which columns are ALL NA (i.e., networks with no patches)
593 naCols <- apply( X=mat2, MARGIN=2, FUN=function(x) all(is.na(x)) )
594 # Select the cols (networks) that contain patches
595 mat3 <- subset( mat2, select=which(naCols==FALSE) )
596 # Return mat: all patches are in one (and only one) network, and all
597 # networks have (at least) one node
598 return( mat3 )
599 } # End RemoveDupPatches function

600 # If minDistMat is not all NA
601 if( !all(is.na(minDistMat)) ) {
602   # Get the subset of patches and networks with patches
603   patchNetwork <- RemoveDupPatches( mat=minDistMat )
604 } # End if is not all NA

605 # If minDistMat is all NA, set patchNetwork to a 0x0 matrix
606 if( all(is.na(minDistMat)) ) patchNetwork <- matrix( NA, nrow=0, ncol=0 )
607
608 # Finally, combine the distance matrices from each subset
609 CombineDistances <- function( dat ) {
610   # Initialize the big matrix to hold all the pairwise distances
611   mat <- matrix( NA, nrow=nrow(patchesUTM), ncol=nrow(patchesUTM) )
612   # Set up row and columns indices for the top left corner of the big matrix
613   iRC <- 1
614   # Initialize a vector to hold point names
615   ptNames <- vector( )
616   # Loop over data subsets
617   for( i in 1:length(dat) ) {
618     # Load the distance matrix
619     load( file=paste("RDataOutTemp/distMat.", dat[i], ".RData", sep="") )
620     # Get the right column (network) from patchNetwork
621     iCol <- which( colnames(patchNetwork) == dat[i] )
622     # Get the rows that indicate the network's patches
623     iRows <- which( is.na(patchNetwork[, iCol]) == FALSE )
624     # Get the names of patches from patchNetwork (these are the only ones that
625     # should be in distMat
626     pnPatches <- rownames( patchNetwork )[iRows]
627     # Check that distMat doesn't have patches that aren't supposed to be in
628     # a different (i.e., closer) network
629     if( all( colnames(distMat) %in% pnPatches) == FALSE ) {
630       # Determine which patches should be included
631       inclPatch <- which( colnames(distMat) %in% pnPatches )
632       # Subset distMat to include only patches that should be in the network
633       distMat <- distMat[inclPatch, inclPatch]
634       # If distMat is now empty (i.e., there is only one patch) ensure that
635       # it's a matrix with 1 row and 1 column with correct names and
636       # distance=0
637       if( all(distMat == 0) ) {
638

```

```

641      # Make the matrix
642      distMat <- matrix( 0, nrow=1, ncol=1 )
643      # Give it column and row names
644      rownames( distMat ) <- pnPatches
645      colnames( distMat ) <- pnPatches
646    } # End if distMat is zero
647  } # End if there are extra patches in distMat
648  # If there is data in distMat, append the distances and names
649  if( !is.null(dim(distMat)) ) {
650    # Get the number of rows
651    nr <- nrow( distMat )
652    # If there are rows, get data
653    if( nr >= 1 ) {
654      # Append the names to the vector
655      ptNames[iRC:(iRC+nr-1)] <- rownames( distMat )
656      # Append distMat to the big matrix
657      mat[(iRC:(iRC+nr-1)), (iRC:(iRC+nr-1))] <- distMat
658      # Update index for rows and columns
659      iRC <- iRC + nr
660    } # End if there are rows
661  } # End if distMat had data
662 } # End loop over subsets
663 # Remove empty rows
664 mat <- matrix( mat[(1:length(ptNames)), (1:length(ptNames))],
665                 nrow=length(ptNames) )
666 # If there are rows and columns
667 if( !is.null(dim(mat)) ) {
668  # Add row and column names
669  rownames( mat ) <- ptNames
670  colnames( mat ) <- ptNames
671 } # End if there are rows and columns
672 # Return the distance matrix
673 return( mat )
674 } # End CombineDistances function

675 # Run this function if there is at least one row in patchNetwork (i.e., there
676 # is at least one point in the area). This only needs to be done for networks
677 # that have patches (i.e., columns in the object patchNetwork)
678 if( dim(patchNetwork)[1] >= 1 ) {
679  pairDists <- CombineDistances( dat=colnames(patchNetwork) )
680 } # End if there are points
681
682 # If there are zero points, the pairDists matrix is 0x0.
683 if( dim(patchNetwork)[1] == 0 ) pairDists <- matrix( NA, nrow=0, ncol=0 )

684 # Collect garbage
685 gc( )
686
687 # Fill in the pairDists matrix with NA if any patches were omitted
688 FillPairDists <- function( mat ) {
689  # Get indices for the missing sites
690  indMissing <- which( !patches$Site %in% colnames(mat) )
691  # Get missing site names
692  noPatch <- patches$Site[indMissing]
693  # Set up a matrix for columns
694  colMat <- matrix( NA, nrow=nrow(mat), ncol=length(noPatch) )
695  # Give it names
696  colnames( colMat ) <- noPatch
697  # Append cols
698  mat <- cbind( mat, colMat )
699  # Set up a matrix for rows
700  rowMat <- matrix( NA, nrow=length(noPatch), ncol=ncol(mat) )
701  # Give it names
702  rownames( rowMat ) <- noPatch
703  # Append rows

```

```

705 mat <- rbind( mat, rowMat )
# Return the new table
707 return( mat )
} # End FillPairDists function
709
# Check if all the sites are in pairDists
711 if( !all( patches$Site %in% colnames(pairDists) ) ) {
# If not, run the function
713 pairDists <- FillPairDists( mat=pairDists )
} # End if there are missing sites
715
# Order pairDists so that patches are in the original order
717 pairDists <- pairDists[mixedsort(colnames(pairDists)),
  mixedsort(colnames(pairDists))]
719
# Convert distances from m to km (to conform with GRIP2 and RAMAS); it is
721 # *crucial* that users verify that distances are in the correct units!
pairDists <- pairDists / 1000
723
# Set the diagonal (i.e., from the patch to itself) from 0.0 to NA (to
725 # conform with GRIP2 and RAMAS)
diag( pairDists ) <- NA
727
# Save the habitat patches
729 save( patches, patchesUTM,
  file=paste("RDataOutDist/patches.", y, ".RData", sep="") )
731
# Save the pairwise distances with index y in newNreps
733 save( pairDists, file=paste("RDataOutDist/pairDists.", y, ".RData", sep="") )
735 # Save the matrices indicating patches, networks, and distances snapped
save( minDistMat, patchNetwork,
737   file=paste("RDataOutDist/patchNetworkDist.", y, ".RData", sep="") )
739 #####
#### End of file 'NetworkDistances.R' #####
#####
741

```

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